

# **Unit 6**

## **Molecular Biology**

### **Chapter 13: The Molecular Basis of Inheritance**

# Evidence that DNA is the genetic material

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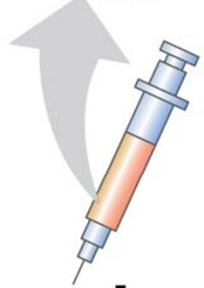
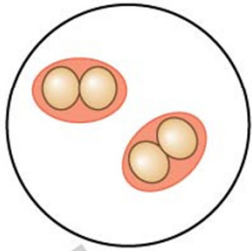
## Experiments:

- Frederick Griffith discovered **transformation**
  - Now defined as a change in genotype and phenotype due to assimilation of foreign DNA
  - Worked with two strains of a bacterium, one pathogenic and one harmless
  - When he mixed heat-killed remains of the pathogenic strain with living cells of the harmless strain, some living cells became pathogenic
- Oswald Avery and others identified the transforming substance as DNA

Figure 13.2

## Experiment

**Living  
S cells  
(control)**

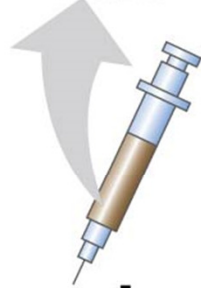
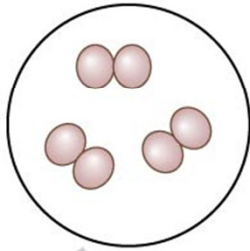


## Results

**Mouse dies**



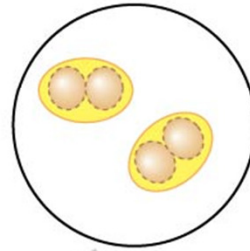
**Living  
R cells  
(control)**



**Mouse healthy**



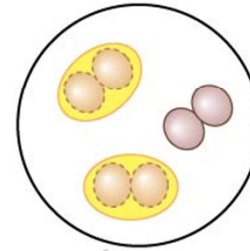
**Heat-killed  
S cells  
(control)**



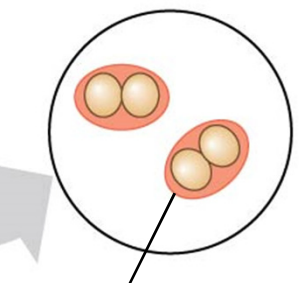
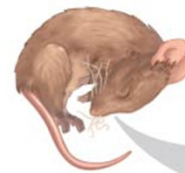
**Mouse healthy**



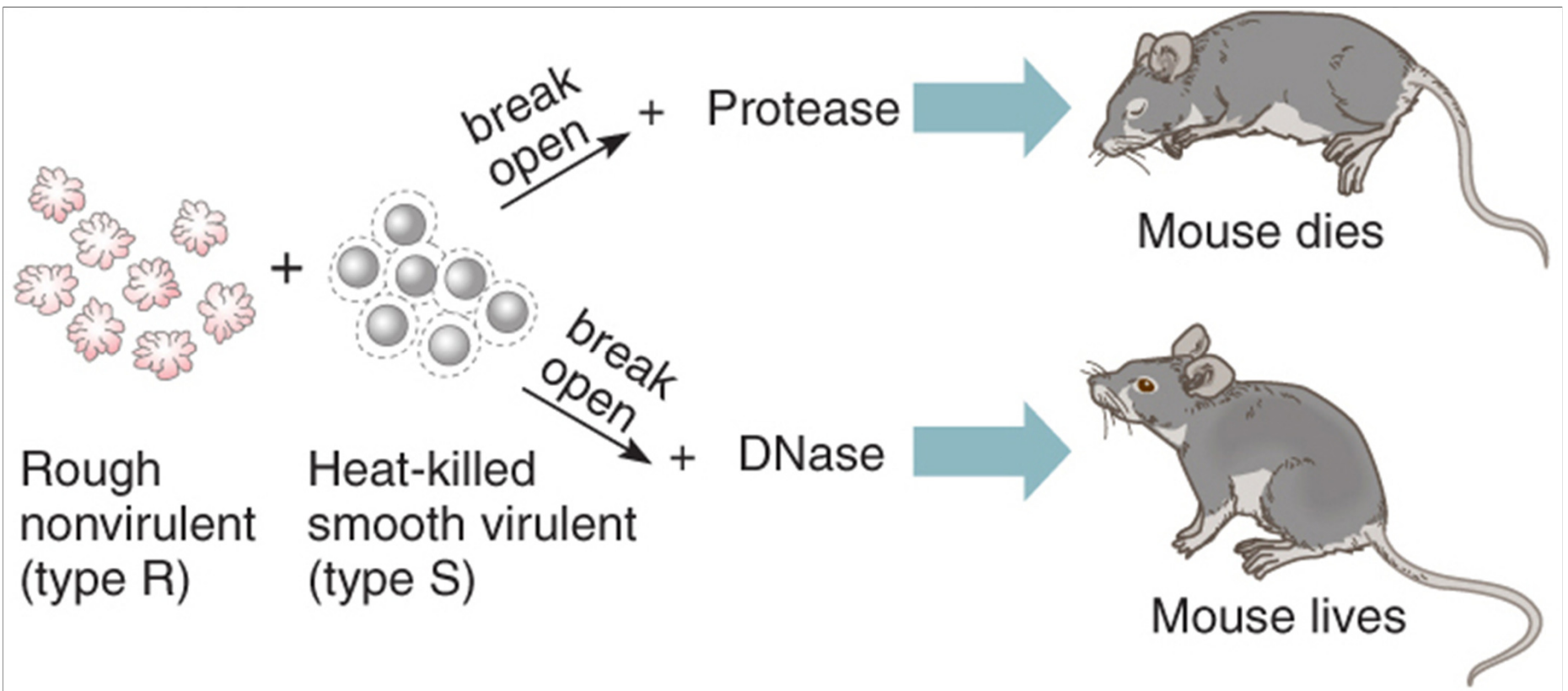
**Mixture of  
heat-killed  
S cells and  
living R cells**



**Mouse dies**



**Living S cells**



- 
- Hershey and Chase showed that DNA is the genetic material of a **bacteriophage**
    - Virus that infects bacteria
    - Used radioactive isotopes of
      - Sulfur to tag protein
      - Phosphorus to tag DNA
    - Showed that only the DNA, and not the protein, enters an *E. coli* cell during infection

Figure 13.4

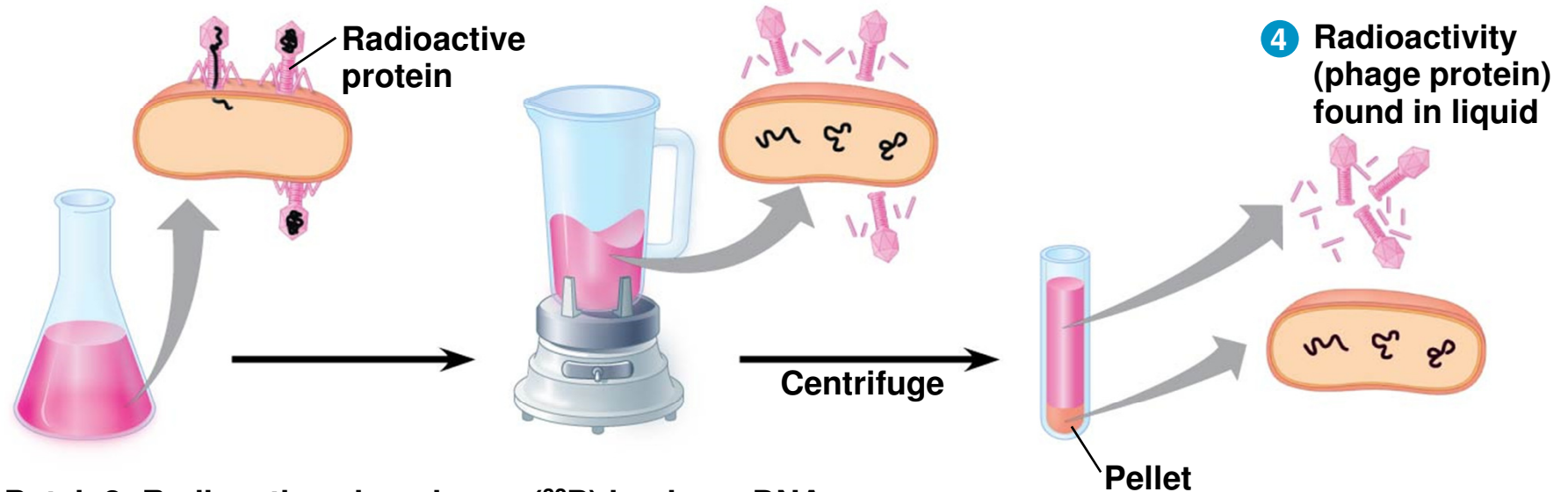
## Experiment

### Batch 1: Radioactive sulfur ( $^{35}\text{S}$ ) in phage protein

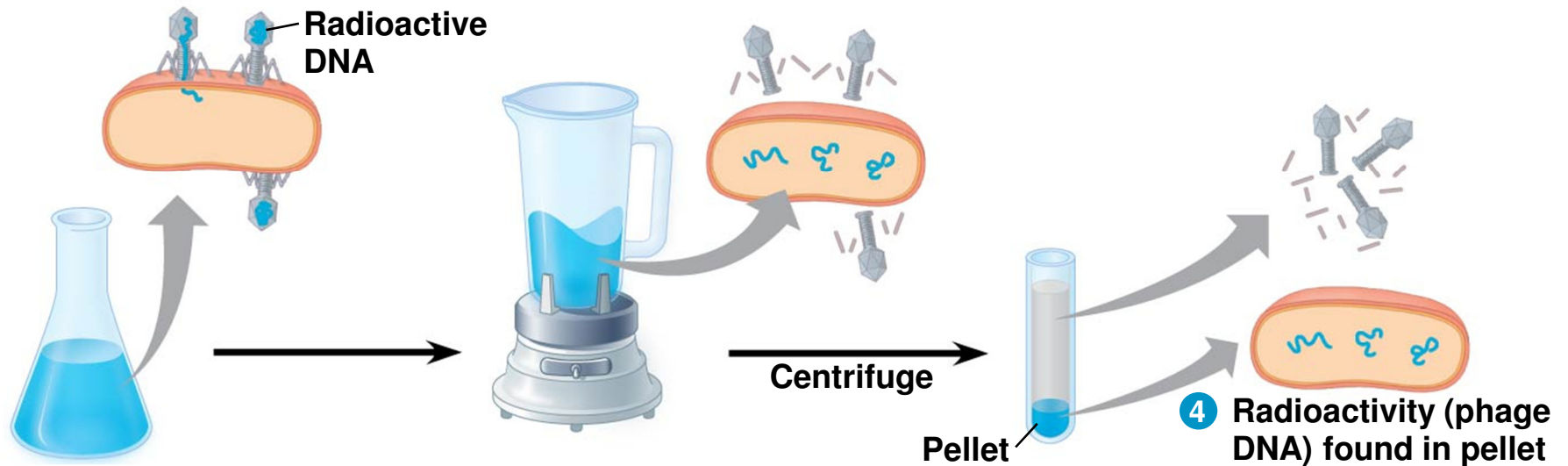
1 Labeled phages infect cells.

2 Agitation frees outside phage parts from cells.

3 Centrifuged cells form a pellet.



### Batch 2: Radioactive phosphorus ( $^{32}\text{P}$ ) in phage DNA



- 
- It was known that DNA is a polymer of nucleotides, each consisting of 3 components:
    - A nitrogenous base
    - A sugar
    - A phosphate group
  - Chargaff found that
    - The base composition of DNA varies between species
    - In any species the number of A and T bases is equal and the number of G and C bases is equal
    - EX: If 40% of a sample of DNA is adenine, how much is cytosine?

- 
- Maurice Wilkins and Rosalind Franklin produced a picture of DNA using X-ray crystallography
  - Those images led James Watson and Francis Crick were first to determine the structure of DNA is a **double helix**
    - Two outer sugar-phosphate backbones
      - **Antiparallel**
        - Their subunits run in opposite directions
    - Nitrogenous bases paired in the molecule's interior



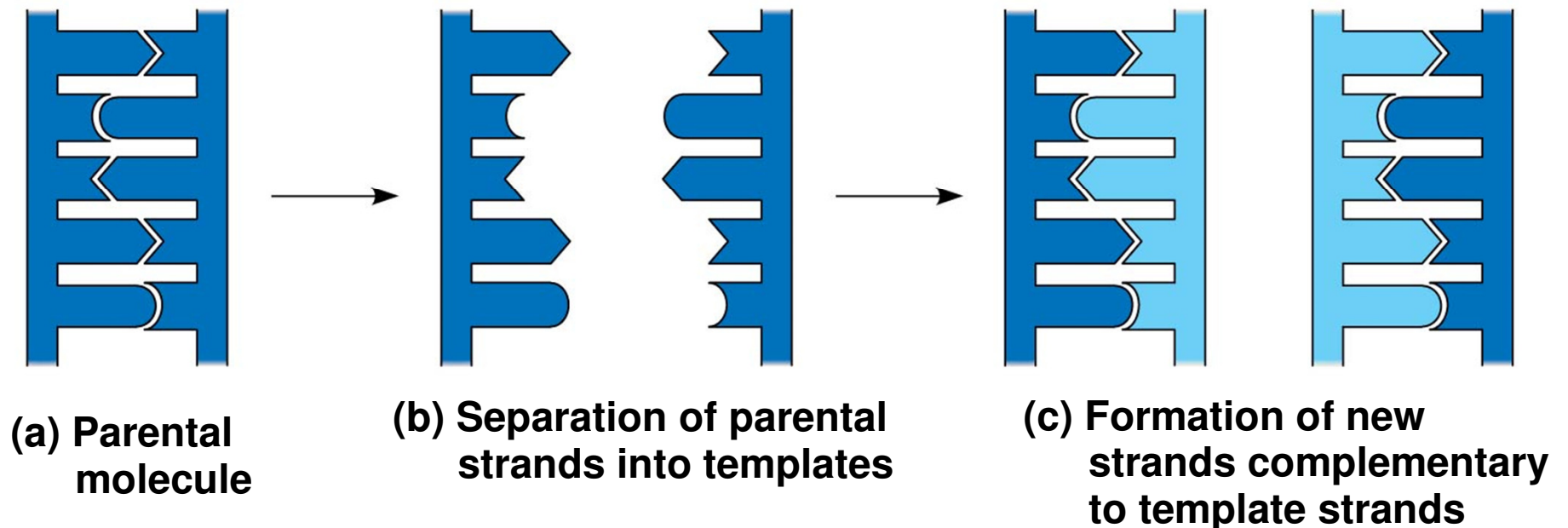
- 
- Purines have 2 organic rings
    - Guanine
    - Adenine
  - Pyrimidines have single ring
    - Cytosine
    - Thymine
  - They determined
    - Adenine (A) paired only with thymine (T)
    - Guanine (G) paired only with cytosine (C)
      - Explains Chargaff's rules!

# DNA Replication

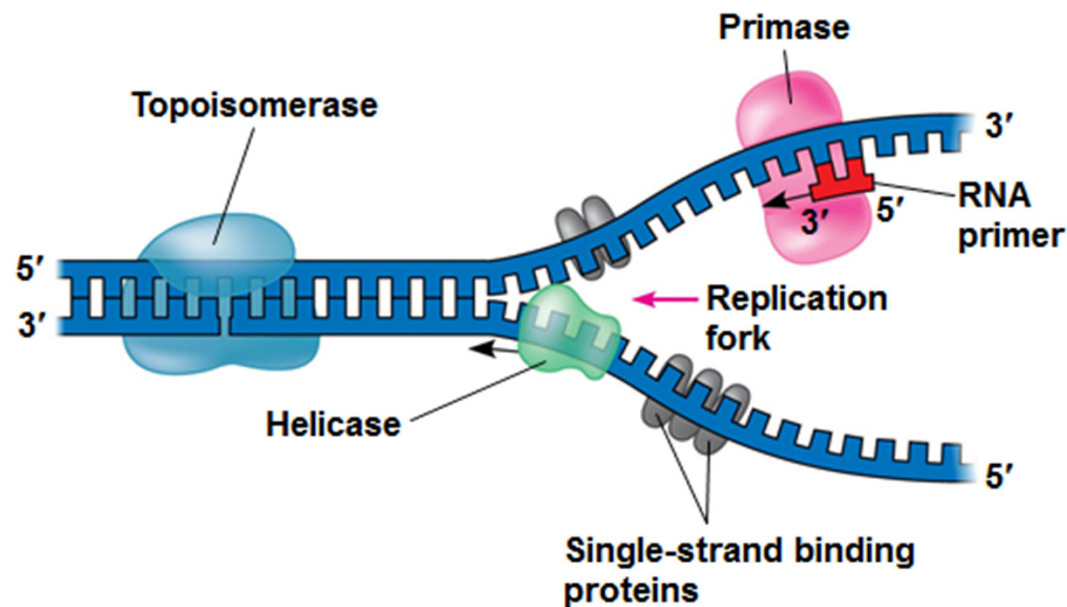
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- DNA is copied during **DNA replication**
  - Occurs during S phase of interphase
- Since the two strands of DNA are ***complementary***, each strand acts as a template for building a new strand in replication
- In DNA replication, the parent molecule unwinds, and two new daughter strands are built based on base-pairing rules

- 
- Watson and Crick's prediction was for a **semiconservative model** of replication
    - When a double helix replicates, each daughter molecule will have one old strand (derived or “conserved” from the parent molecule) and one newly made strand



- Replication begins at **origins of replication**
  - Here, the two DNA strands are separated, opening up a replication “bubble”
- At each end of a bubble is a **replication fork**
  - A Y-shaped region where the parental strands of DNA are being unwound



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- Prokaryotes

- Typically have one circular chromosome
- Has single origin in replication, forming one replication bubble
- Replication proceeds in both directions until entire molecule is copied

- Eukaryotes

- Have hundreds to thousands of replication origins
- Multiple replication bubbles form and eventually fuse
  - Speeds up the copying of DNA
- Replication proceeds in both directions from each origin

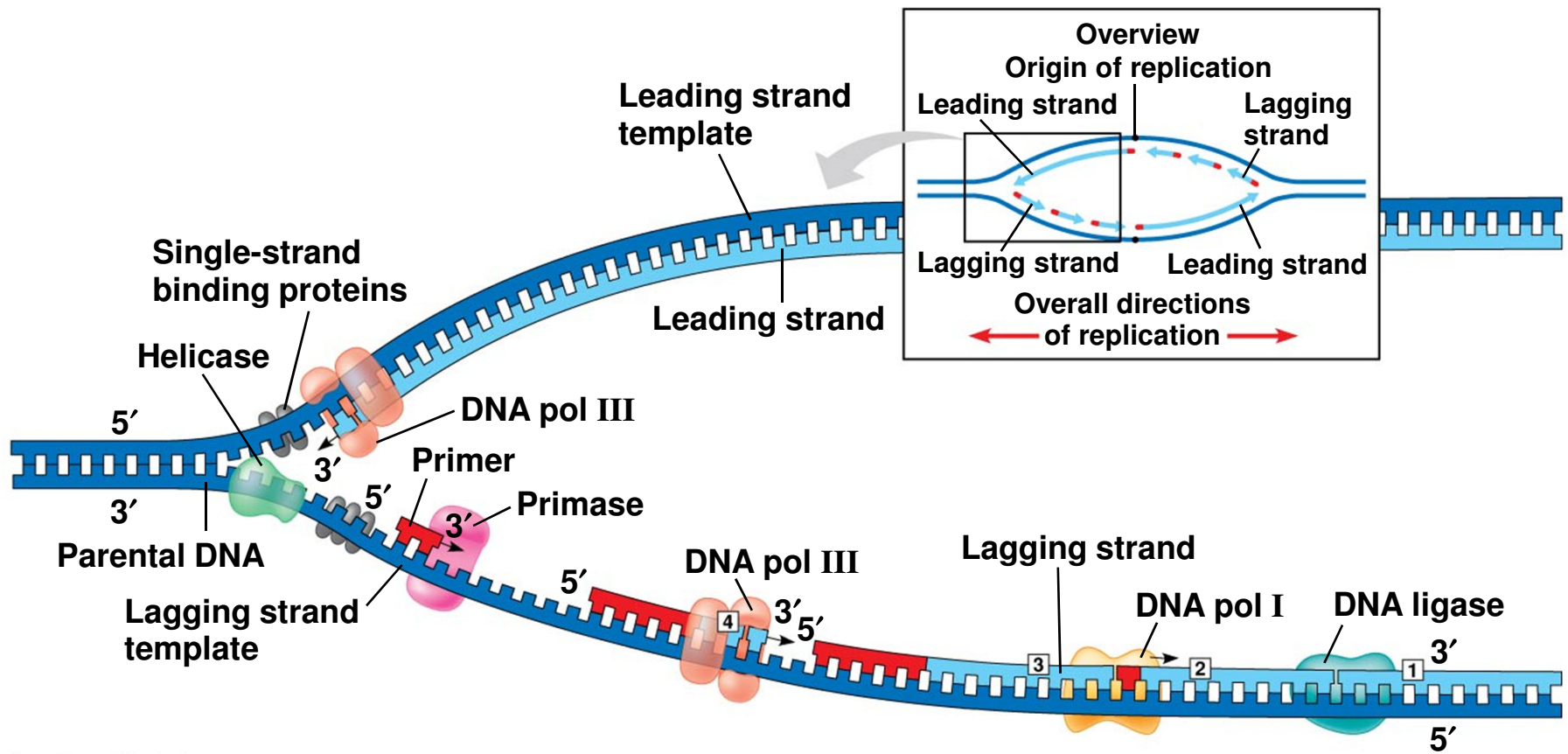
# Enzymes involved in DNA Replication

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- **Helicases** are enzymes that untwist the double helix at the replication forks
- **Single-strand binding proteins** bind to and stabilize single-stranded DNA
- **Topoisomerase** relieves the strain caused by tight twisting ahead of the replication fork by breaking, swiveling, and rejoining DNA strands
- **Primase** adds a short RNA primer

- 
- **DNA polymerase** catalyzes the elongation of the new DNA strand
    - Can only add nucleotides to the free 3' end of a growing strand
    - Therefore, a new DNA strand can elongate only in the 5' to 3' direction!
      - **Leading strand** is synthesized continuously, moving toward the replication fork
      - **Lagging strand** is synthesized as a series of segments called **Okazaki fragments**
        - Because DNA is **antiparallel**!
  - **DNA ligase** joins the fragments together

Figure 13.17





# Genetic Engineering

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- **Genetic engineering** = the direct manipulation of genes for practical purposes
  - Applications include agriculture, criminal law, medical research
- **Polymerase chain reaction, or PCR**
  - Can produce many copies of a specific target segment of DNA
    - Fast and specific
  - Used to provide specific DNA fragment to be cloned

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## ■ Recombinant DNA

- DNA from one source is inserted into a bacterial **plasmid**
  - Small circular DNA molecule that replicates separately from the bacterial chromosome
- Note: Works because genetic code is universal

- 
- Bacterial **restriction enzymes** cut DNA molecules at specific DNA sequences called **restriction sites**
    - Each restriction enzyme is very **SPECIFIC**
    - The same enzyme is used to cut the “foreign” DNA and plasmid DNA at the same restriction site
    - Cut in a staggered manner to produce **sticky ends**
      - Can bond with complementary sticky ends of other fragments
  - DNA ligase seals the 2 pieces of DNA together

Figure 13.23-3

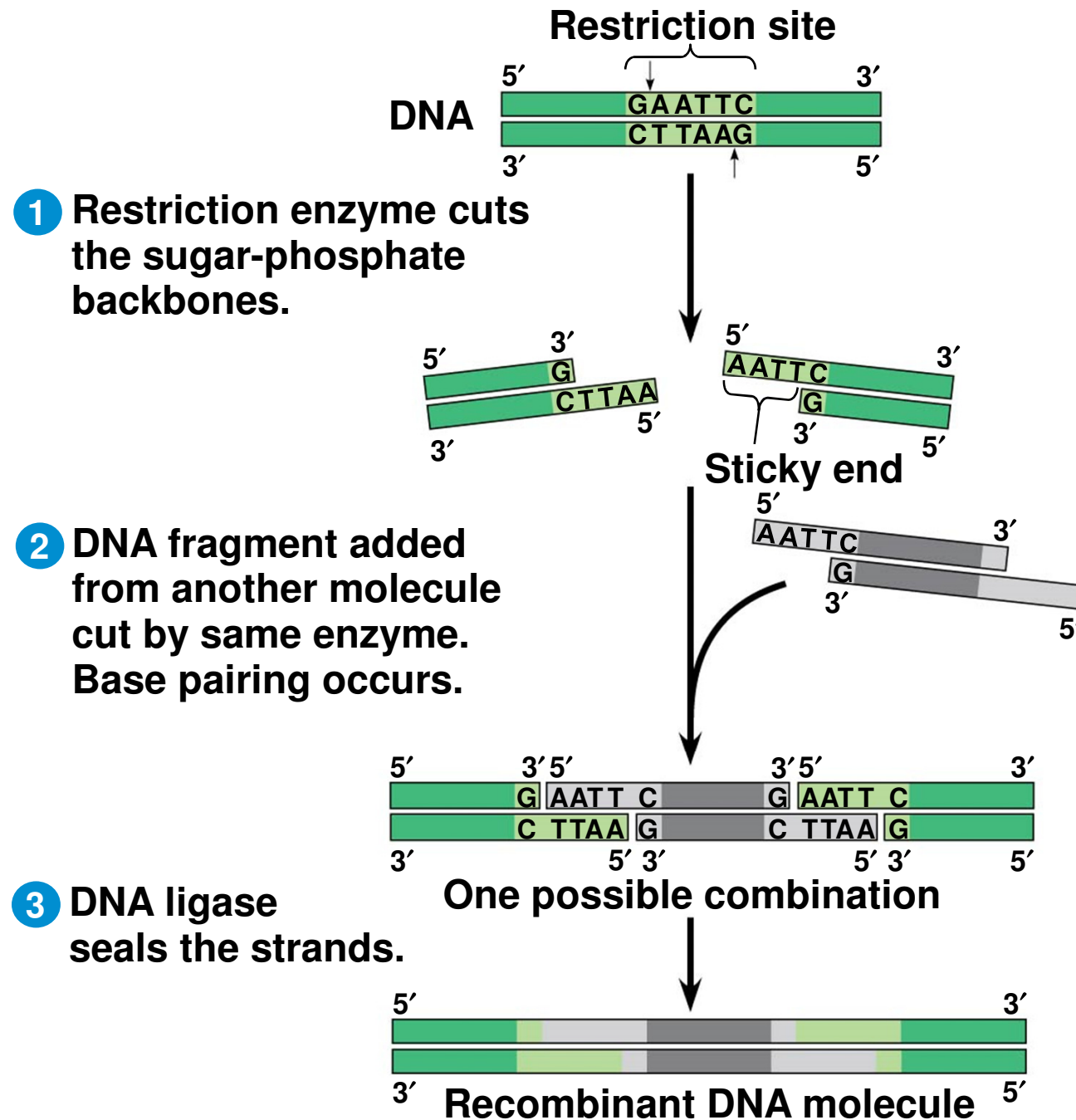


Figure 13.26

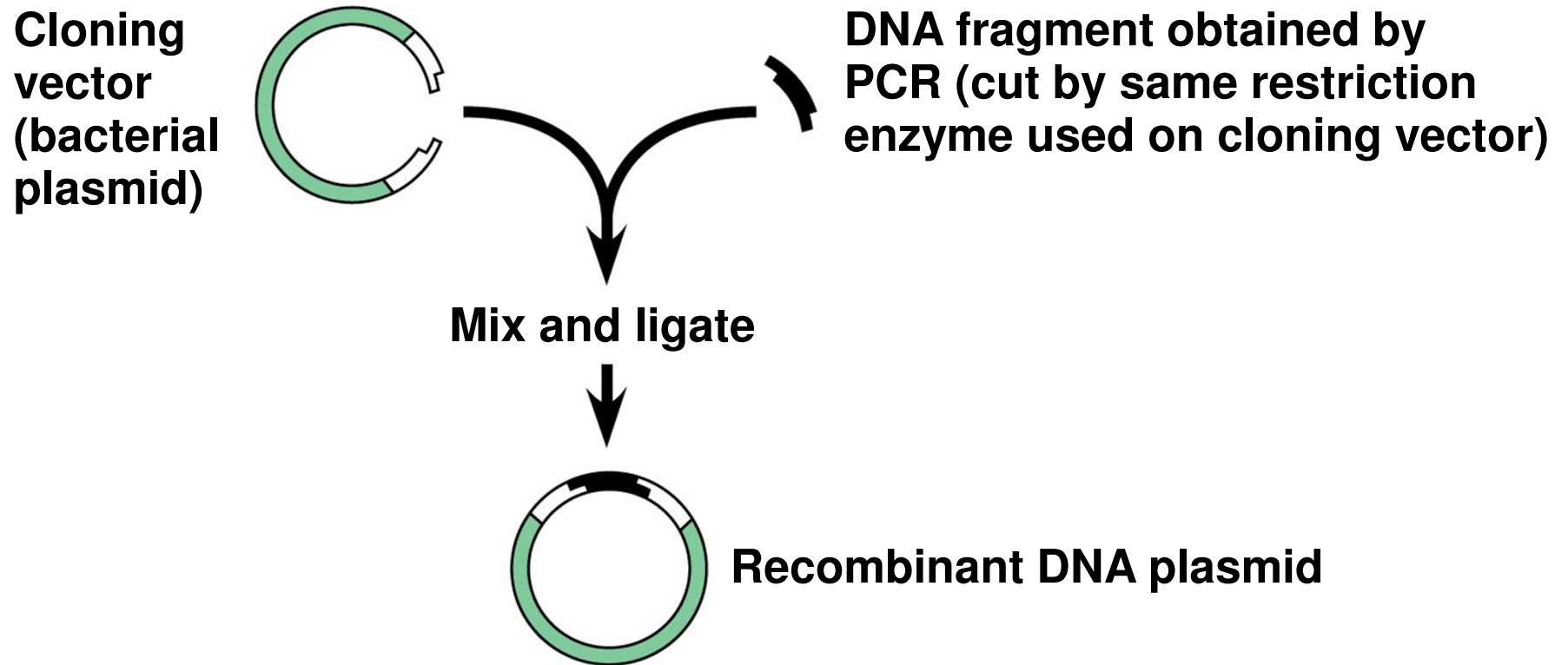
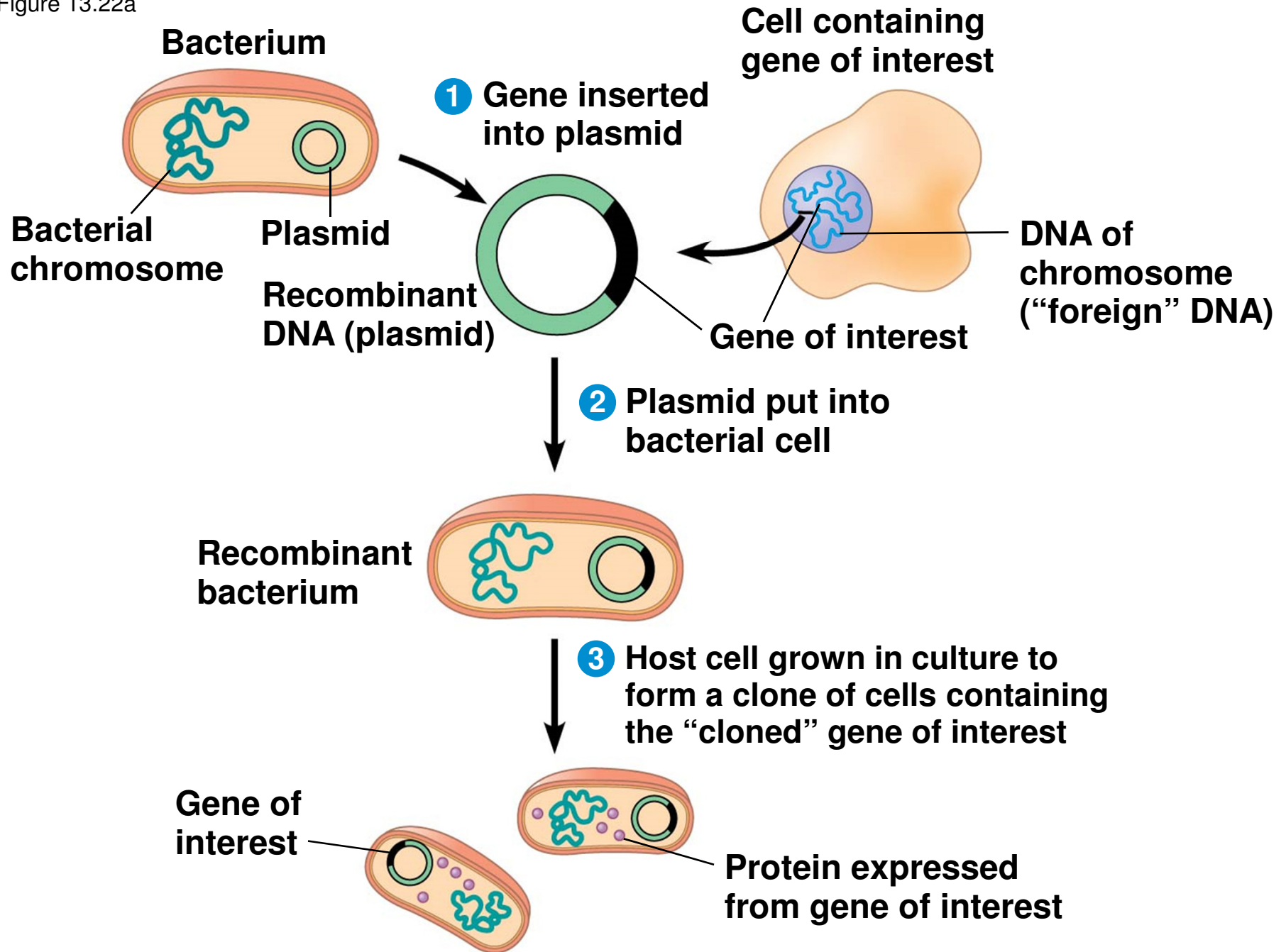


Figure 13.22a

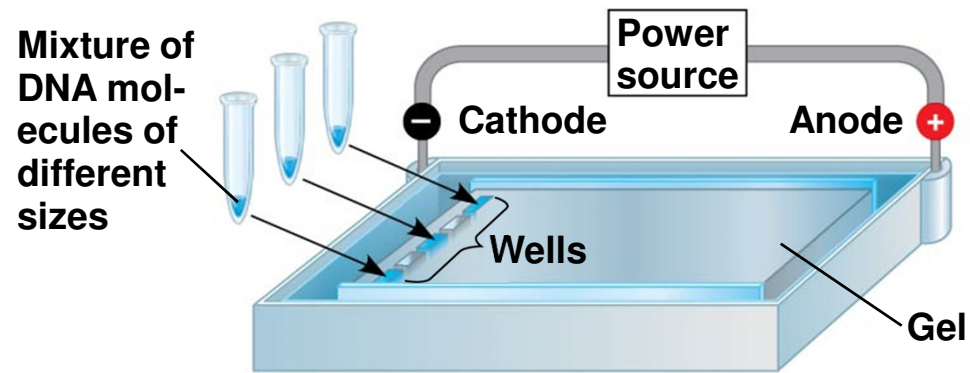


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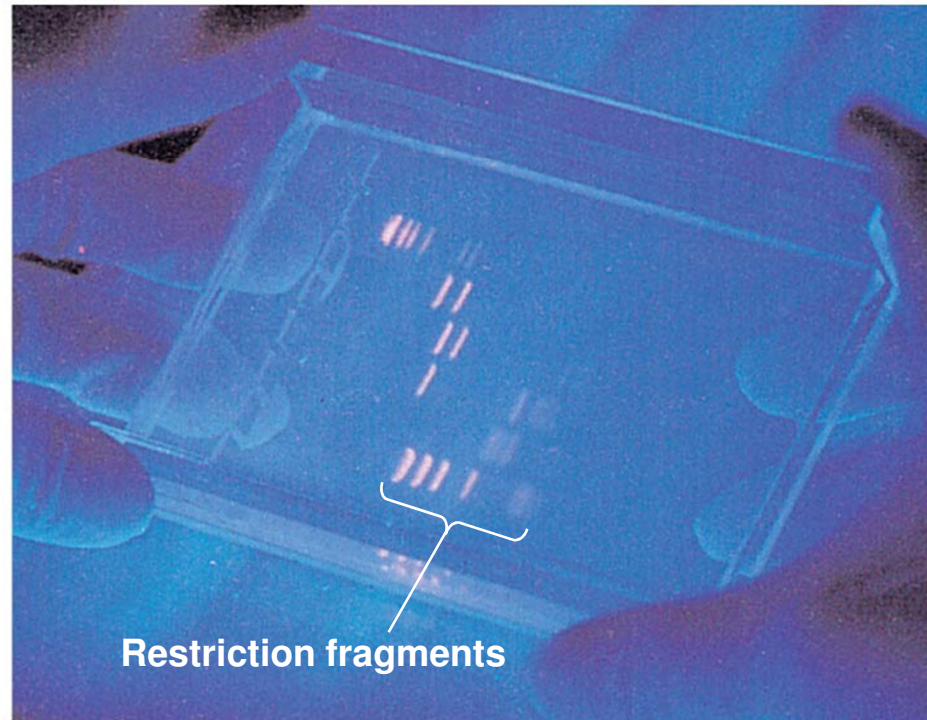
## ■ Gel electrophoresis

- Used to see the fragments produced by cutting DNA molecules with restriction enzymes, researchers use
- This technique separates a mixture of nucleic acid fragments based on length
  - Current is applied to move fragments
    - Negatively charged DNA is loaded in wells at negative end because DNA will move to positive end
  - Smaller fragments move faster (and thus further) than large

Figure 13.24



**(a) Negatively charged DNA molecules will move toward the positive electrode.**



**(b) Shorter molecules are impeded less than longer ones, so they move faster through the gel.**



# **Unit 6**

# **Molecular Biology**

## **Chapter 14: Gene Expression:**

## **From Gene to Protein**

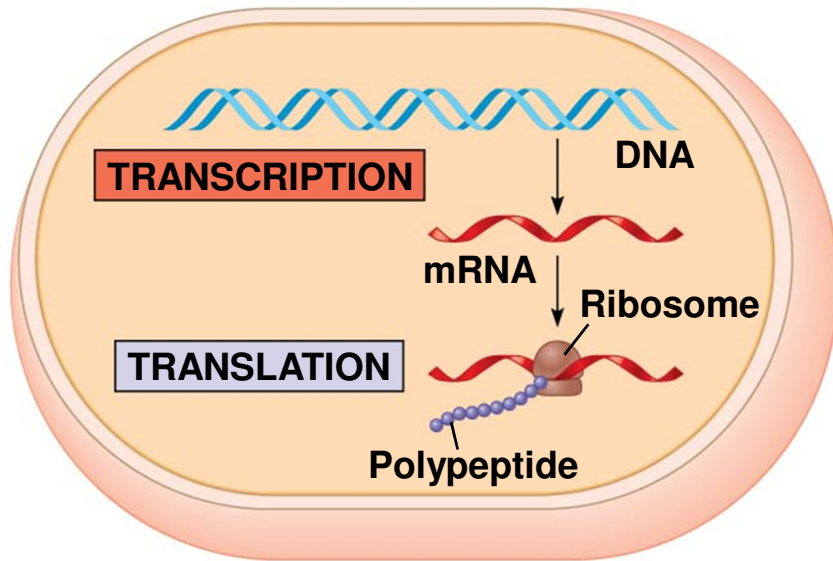
# Gene Expression

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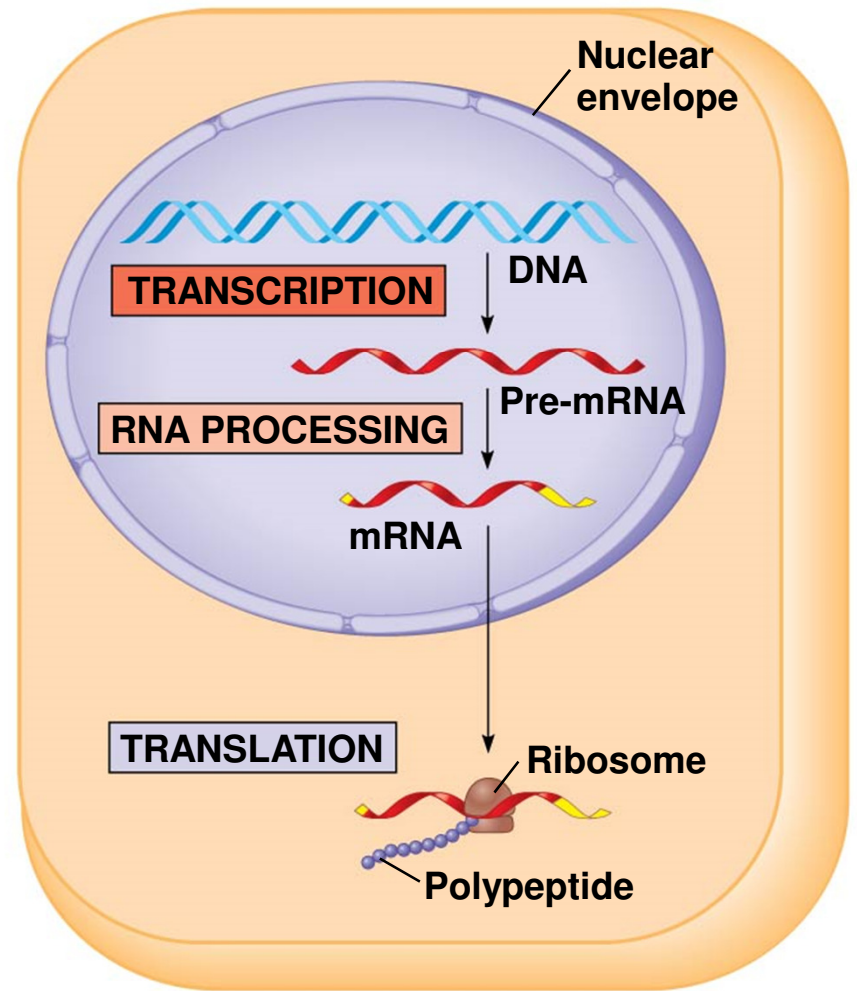
- Genes provide the instructions for making proteins
- Proteins are link between genotype and phenotype
- **Gene expression** is the process by which DNA directs protein synthesis
- Getting from DNA to protein requires two stages:
  - **Transcription** is the synthesis of **mRNA** using information in DNA
    - Occurs in nucleus of eukaryotes
  - **Translation** is the synthesis of a protein, using information in the mRNA
    - Occurs in cytoplasm at ribosomes

- 
- RNA is the bridge between DNA and protein synthesis
  - RNA is chemically similar to DNA, but RNA
    - Has a ribose sugar instead of deoxyribose
    - Has the base uracil (U) rather than thymine (T)
    - Is usually single-stranded

Figure 14.4



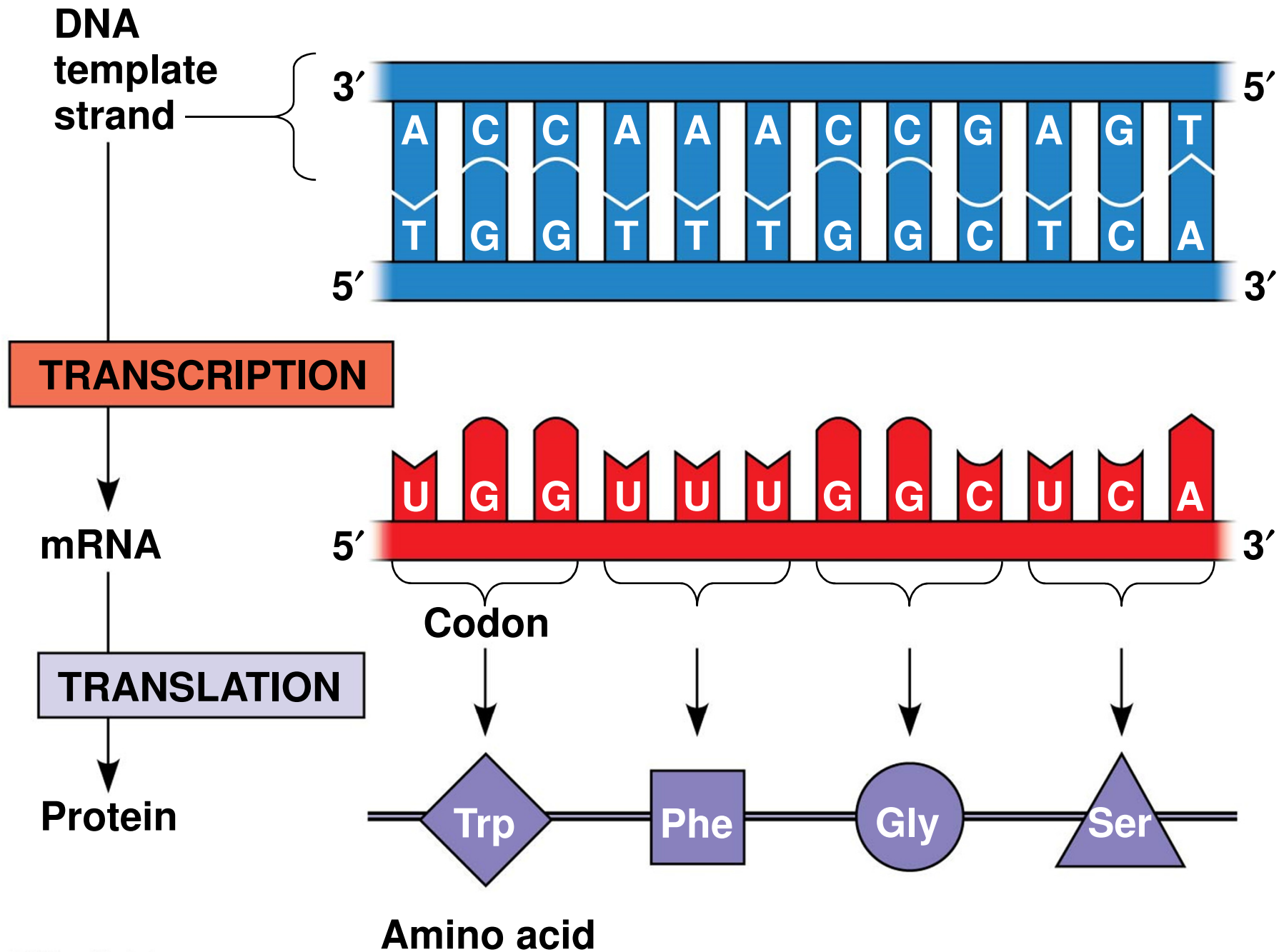
(a) Bacterial cell



(b) Eukaryotic cell

- 
- The flow of information from gene to protein is based on a **triplet code**
    - A series of nonoverlapping, three-nucleotide words
  - The words of a gene are transcribed into complementary nonoverlapping three-nucleotide words of mRNA
    - mRNA base triplets are called **codons**
  - These words are then translated into a chain of amino acids, forming a polypeptide (protein)
  - The genetic code is nearly universal
  - Genes can be transcribed and translated after being transplanted from one species to another

Figure 14.5



# Transcription and Translation Practice

- DNA template strand

3' TACGGTCGTTCGAATATC 5'

- mRNA codons

5' AUG CCA GCA AGC UUA UAG 3'

- tRNA anticodons

UAC GGU CGU UCG AAU AUC

- Amino Acid (remember to use the codons!)

Met Pro Ala Ser Leu (STOP)

Figure 14.6

		Second mRNA base					
		U	C	A	G		
First mRNA base (5' end of codon)	U	UUU	UCU	UAU	UGU	U C A G	Third mRNA base (3' end of codon)
		UUC	UCC	UAC	UGC		
		UUA	UCA	UAA Stop	UGA Stop		
		UUG	UCG	UAG Stop	UGG Trp		
	C	CUU	CCU	CAU	CGU	U C A G	
		CUC	CCC	CAC	CGC		
		CUA	CCA	CAA	CGA		
		CUG	CCG	CAG	CGG		
	A	AUU	ACU	AAU	AGU	U C A G	
		AUC	ACC	AAC	AGC		
		AUA	ACA	AAA	AGA		
		AUG Met or start	ACG	AAG	AGG		
	G	GUU	GCU	GAU	GGU	U C A G	
		GUC	GCC	GAC	GGC		
		GUA	GCA	GAA	GGA		
		GUG	GCG	GAG	GGG		



# Transcription = DNA → RNA

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- Transcription is the first stage of gene expression
  1. Initiation
  2. Elongation
  3. Termination
- RNA synthesis is catalyzed by **RNA polymerase**
  - Assembles nucleotides in the 5' to 3' direction
- The DNA sequence where RNA polymerase attaches is called the **promoter**
- In bacteria, the sequence signaling the end of transcription is called the **terminator**

# *Initiation*

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- Promoters signal the transcriptional **start point**
- In eukaryotes, **transcription factors** mediate the binding of RNA polymerase and the initiation of transcription
- A promoter called a **TATA box** is crucial in forming the initiation complex in eukaryotes

# *Elongation*

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- mRNA is synthesized in the 5' to 3' direction
- As RNA polymerase moves along the DNA, it adds nucleotides to the 3' end of the growing RNA molecule (*complementary* to DNA bases)
  - DNA has G; RNA pairs C
  - DNA has C; RNA pairs G
  - DNA has T; RNA pairs A
  - *DNA has A; RNA pairs U*

# *Termination*

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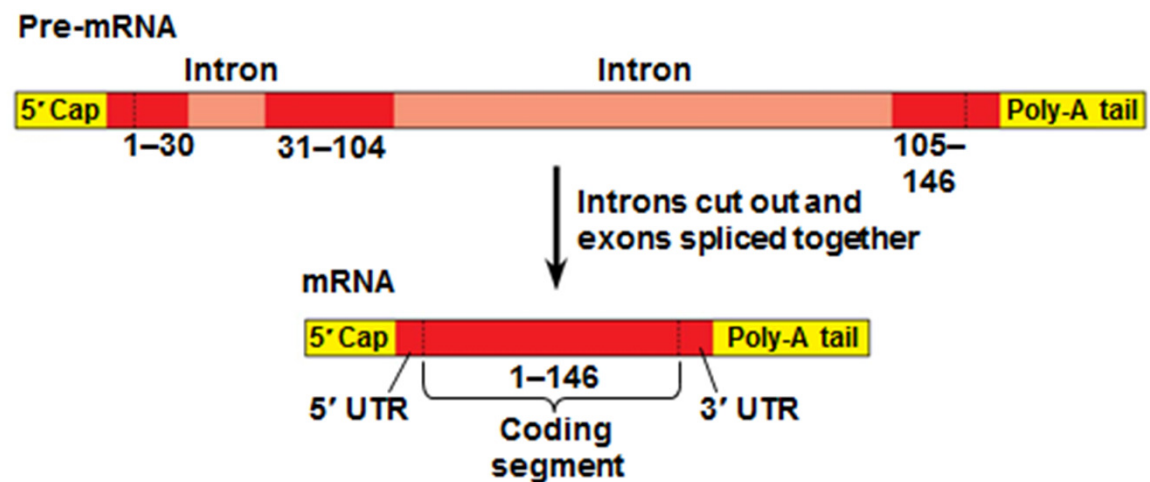
- The mechanisms of termination are different in bacteria and eukaryotes
  - In bacteria
    - The polymerase stops transcription at the end of the terminator
    - mRNA can be translated without further modification
  - In eukaryotes
    - RNA polymerase II transcribes the polyadenylation signal sequence
    - The RNA transcript is released 10–35 nucleotides past this polyadenylation sequence

# RNA Processing

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- In prokaryotes, translation directly follows transcription
  - Steps are not separated by a nucleus
- In eukaryotes, the mRNA is modified after being transcribed before it can be translated
  - **RNA processing**
- Each end of a pre-mRNA molecule is modified in a particular way
  - The 5' end receives a modified **5' cap**
  - The 3' end gets a **poly-A tail**

- Most eukaryotic mRNAs have long noncoding stretches of nucleotides that lie between coding regions
- The noncoding regions are called intervening sequences, or **introns**
- The other regions are called **exons** and are usually translated into amino acid sequences
- **RNA splicing** removes introns and joins exons



- 
- Many genes can give rise to two or more different polypeptides
    - Depending on which segments are used as exons
    - This process is called **alternative RNA splicing**
      - Because of this, the organism's number of different protein products can be much greater than it's number of genes
  - RNA splicing is carried out by **spliceosomes**
    - Complex of proteins and small RNAs that remove introns

# Translation = RNA → Protein

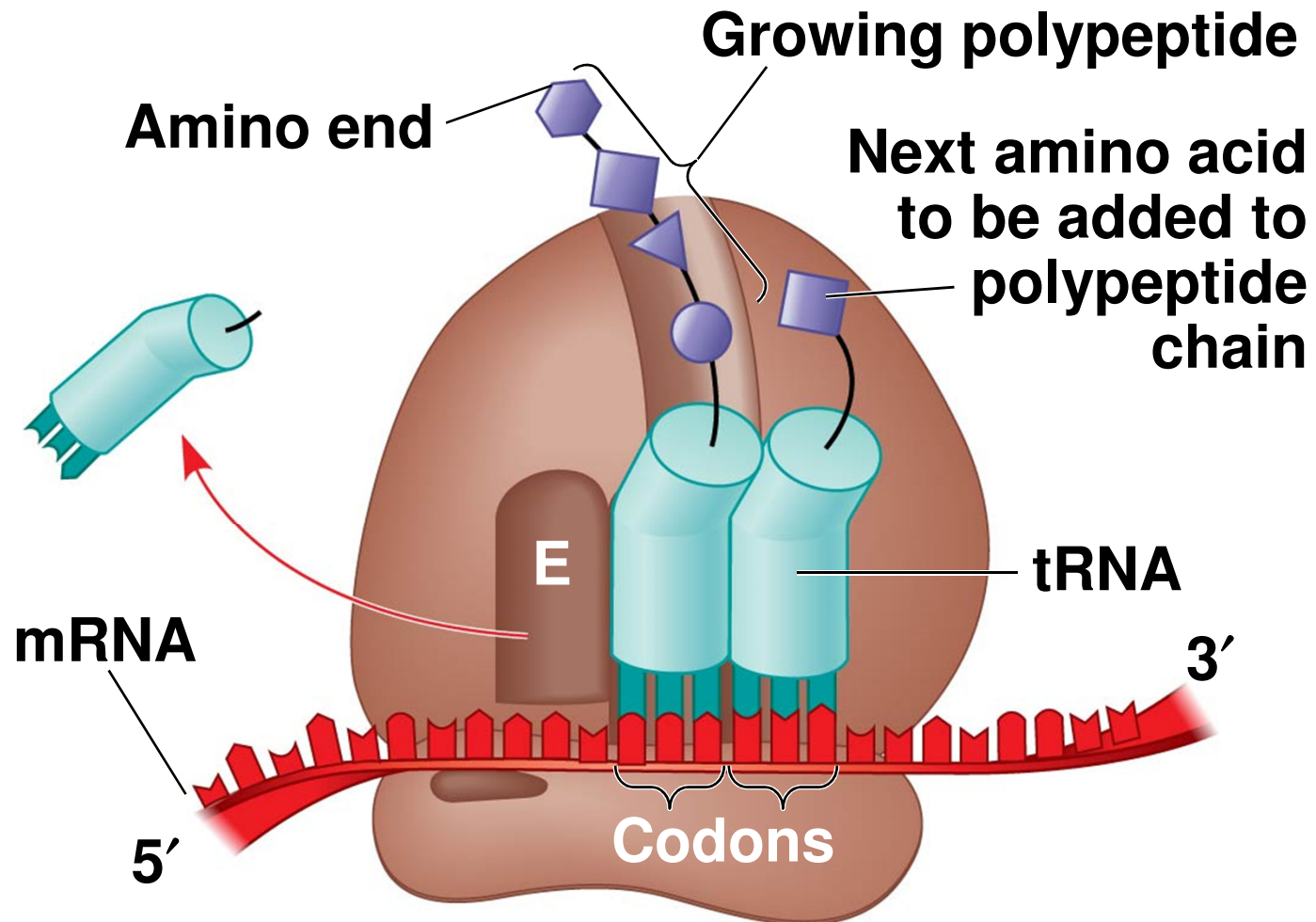
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- Genetic information flows from mRNA to protein through the process of translation
- A cell translates an mRNA message into protein with the help of **transfer RNA (tRNA)**
  - tRNAs transfer amino acids to the growing polypeptide in a ribosome
- One end of the tRNA contains the **anticodon**
  - Nucleotide triplet that pairs with an mRNA codon
- tRNA is a translator
  - Reads a nucleic acid word (mRNA codon)
  - Interprets it as a protein word (amino acid)



- 
- Translation occurs at the ribosomes
    - The large and small ribosomal are made of proteins and **ribosomal RNAs (rRNAs)**
      - Made in nucleolus of eukaryotes
  - A ribosome has three binding sites for tRNA
    - The **P site** holds the tRNA that carries the growing polypeptide chain
    - The **A site** acccepts the tRNA that carries the next amino acid to be added to the chain
    - The **E site** is the exit site, where discharged tRNAs leave the ribosome
  - tRNA moves from A to P to E sites

Figure 14.17c



(c) Schematic model with mRNA and tRNA

# Mutations

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- **Mutations** are changes in genetic material (DNA)
- **Mutagens** are physical or chemical agents that can cause mutations
  - Most cancer-causing chemicals (carcinogens) are mutagenic, and vice-versa
  - Radiation (X-rays and UV rays)
- **Point mutations** are chemical changes in just one or a few nucleotide pairs of a gene

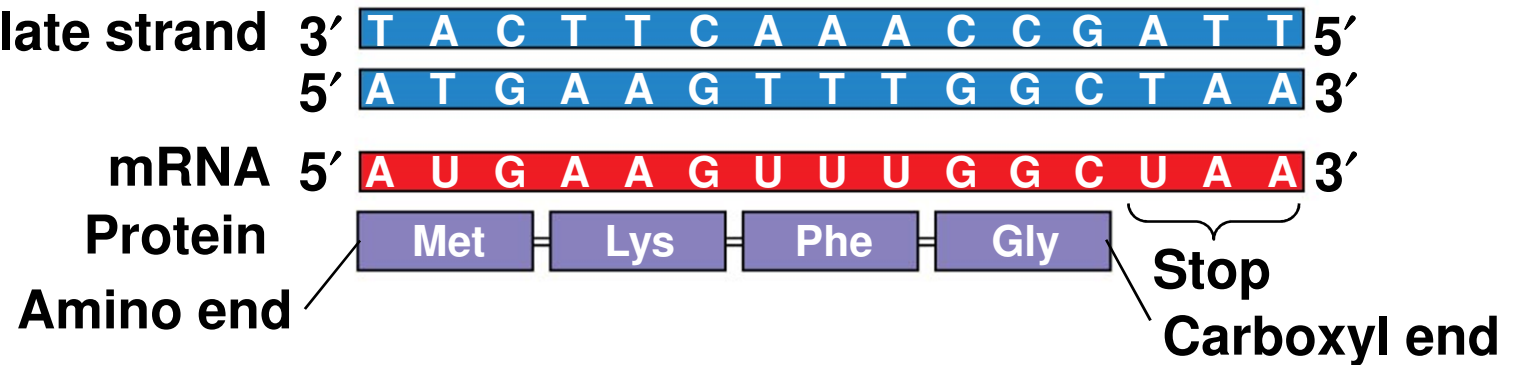
# *Substitutions*

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- A **nucleotide-pair substitution** replaces one nucleotide and its partner with another pair of nucleotides
- **Silent mutations** have no effect on the amino acid produced by a codon because of redundancy in the genetic code
- **Missense mutations** still code for an amino acid, but not the correct amino acid
- **Nonsense mutations** change an amino acid codon into a stop codon
  - Nearly always lead to a nonfunctional protein

Figure 14.26a

## Wild type



Nucleotide-pair substitution:

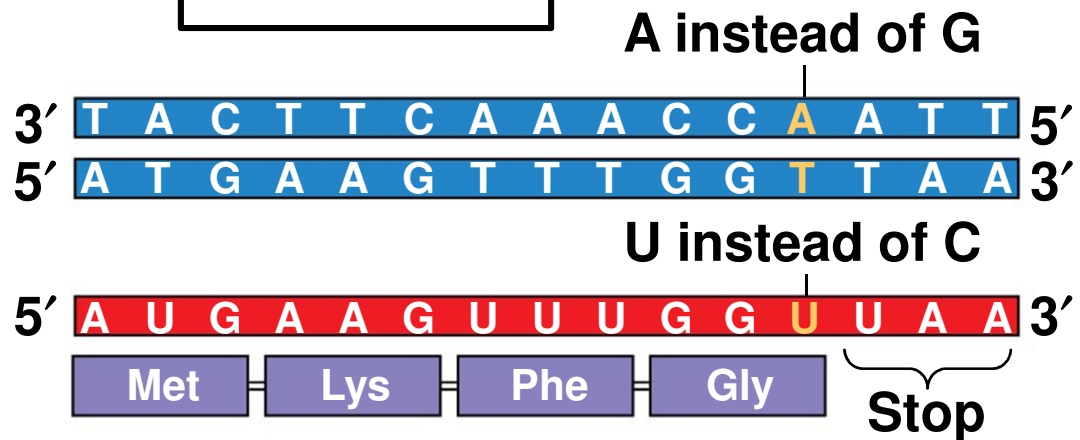
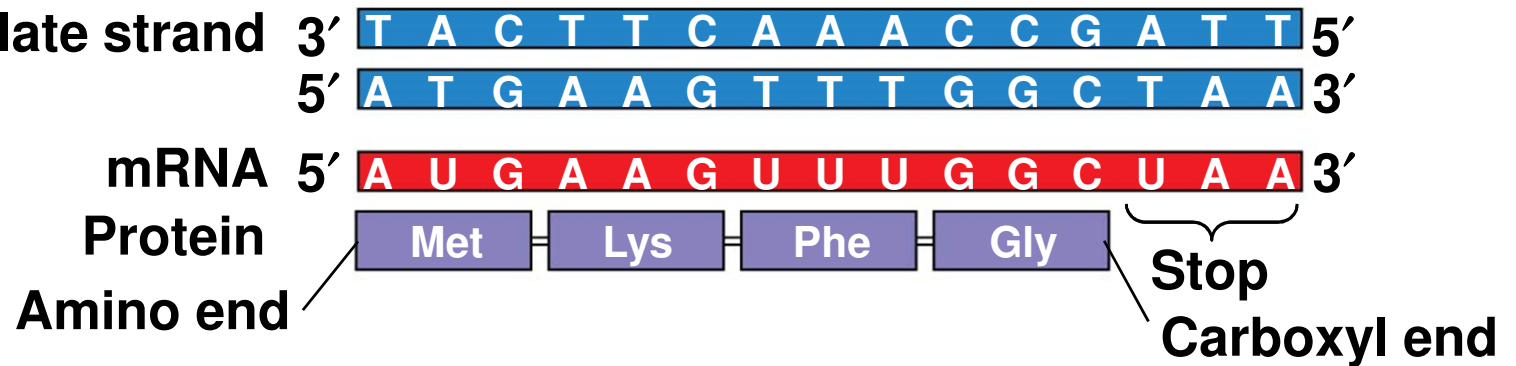


Figure 14.26b

## Wild type



Nucleotide-pair substitution:

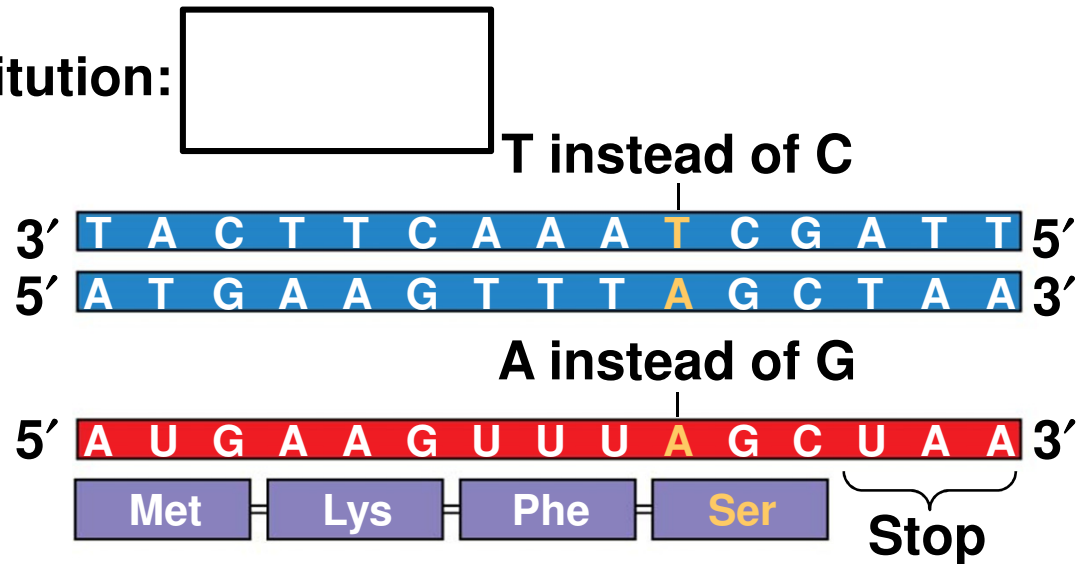
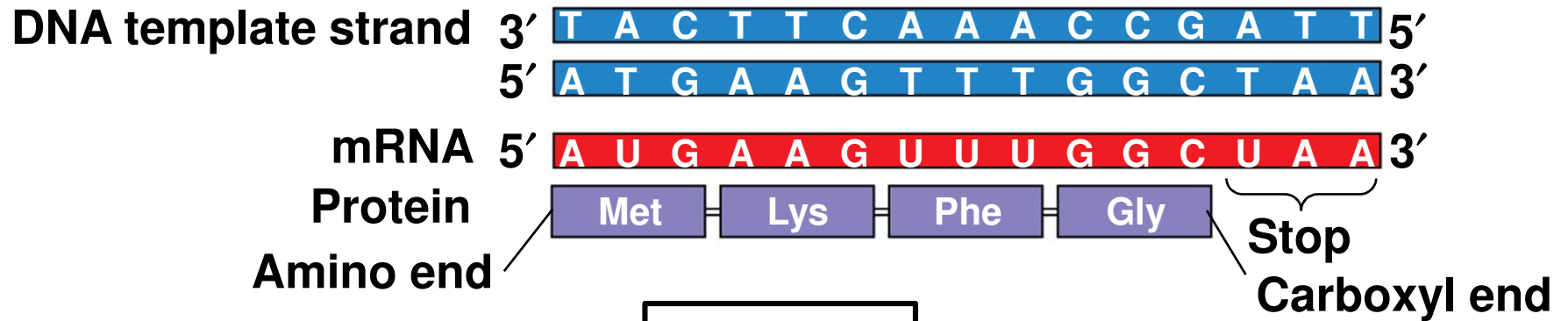
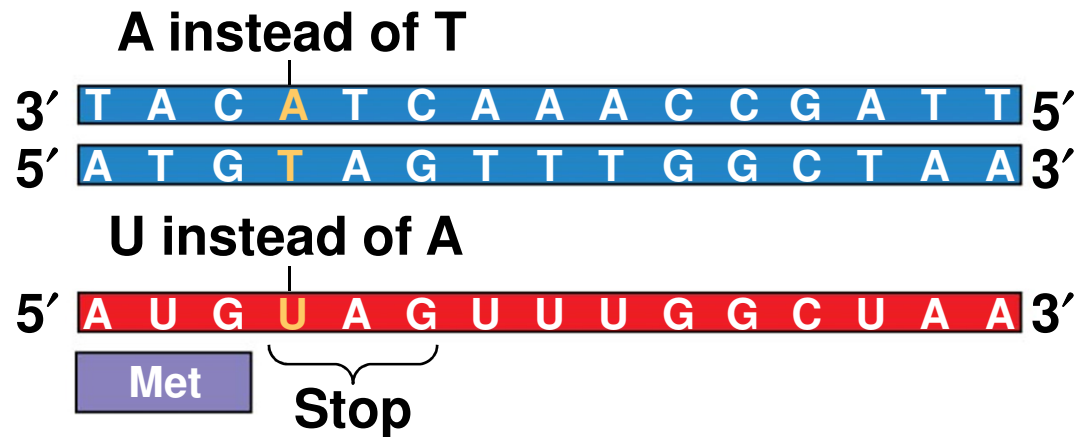


Figure 14.26c

## Wild type



Nucleotide-pair substitution:



# ***Insertions and Deletions***

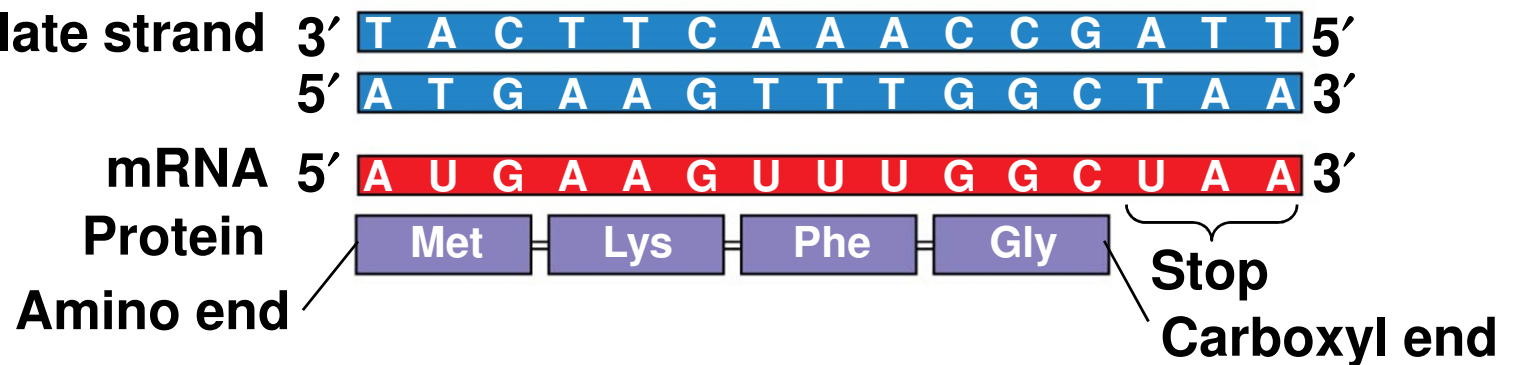
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- **Insertions** and **deletions** are additions or losses of nucleotide pairs in a gene
  - These mutations have a disastrous effect on the resulting protein more often than substitutions do
- Insertion or deletion of nucleotides may alter the reading frame of the genetic message, producing a **frameshift mutation**
  - All of the nucleotides downstream of the deletion or insertion will be improperly grouped into codons
  - Results will be extensive missense
  - Resulting protein is typically nonfunctional
- Note: Inserting or deleting nucleotides in multiples of 3 will NOT shift reading frame
  - But will insert or delete a single amino acid



Figure 14.26d

## Wild type



## Nucleotide-pair insertion: frameshift causing immediate nonsense

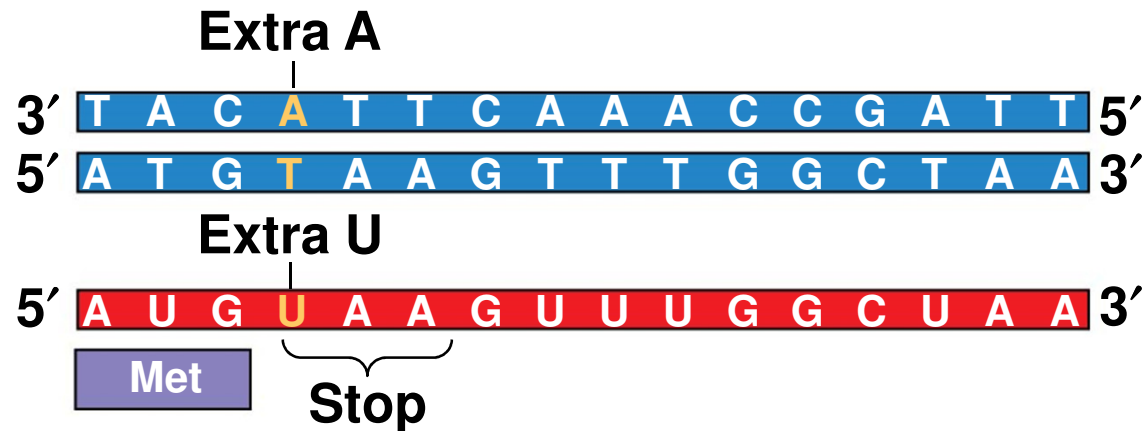
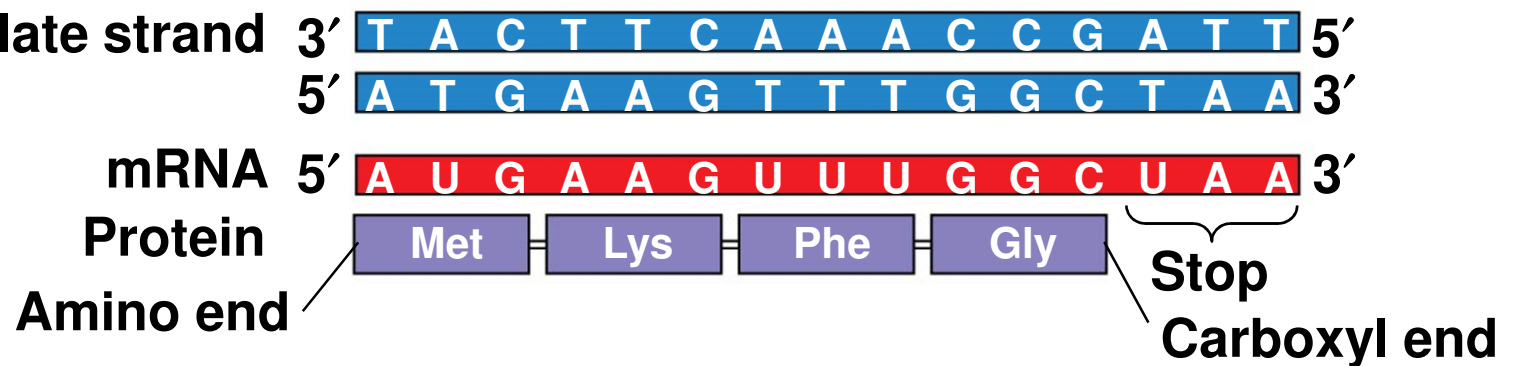


Figure 14.26e

## Wild type



## Nucleotide-pair deletion: frameshift causing extensive missense

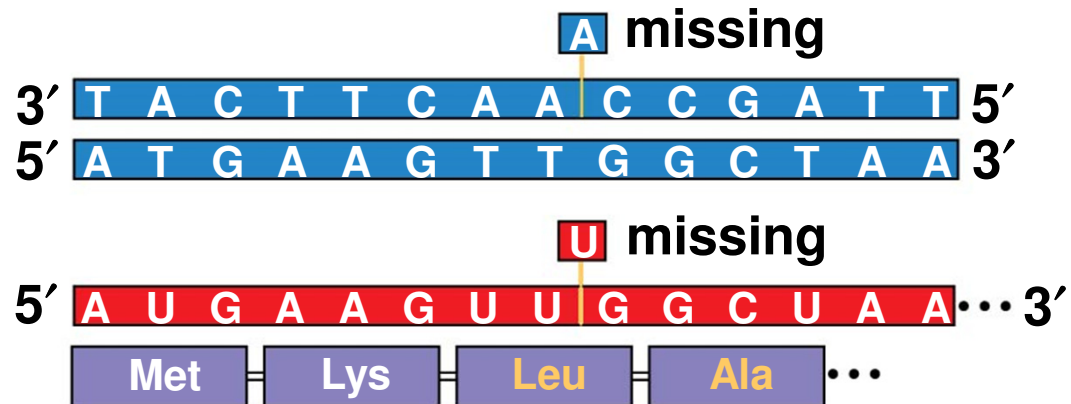
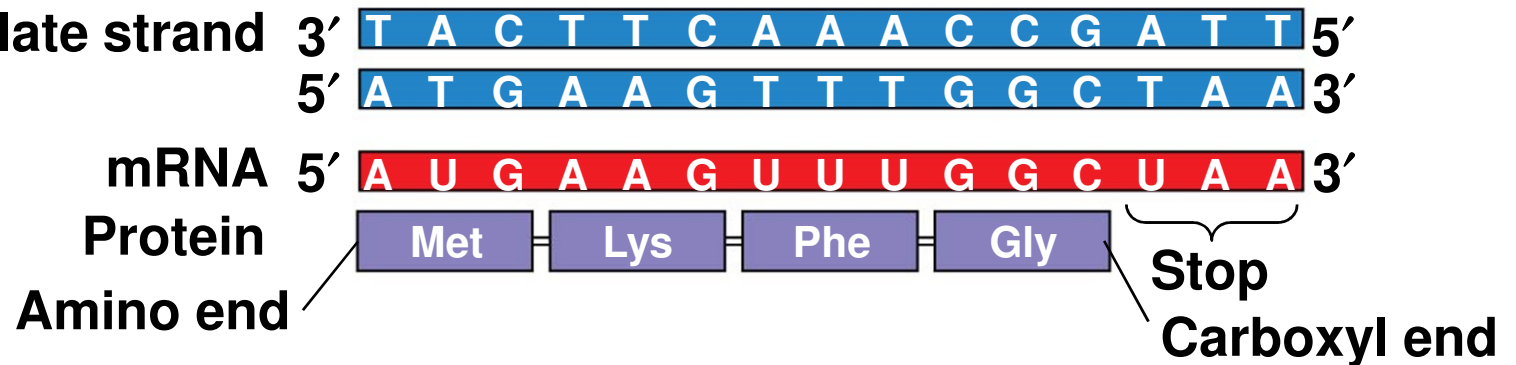
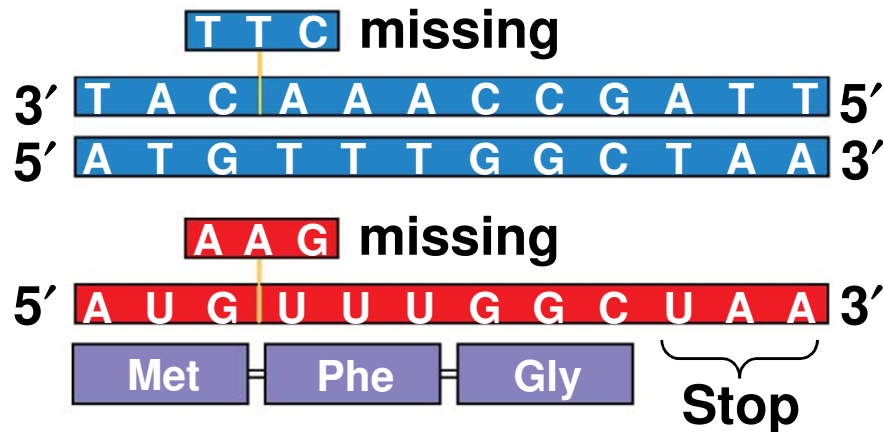


Figure 14.26f

## Wild type



3 nucleotide-pair deletion: no frameshift, but one amino acid missing



# **Unit 6**

# **Molecular Biology**

## **Chapter 15: Regulation of Gene Expression**

# Differential Expression of Genes

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- All of the cells in an organism have the same genome
  - They are just expressed differently!
- Prokaryotes and eukaryotes alter gene expression in response to their changing environment
- Gene expression is often regulated at the transcription stage

# Gene Expression in Bacteria

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- Natural selection has favored bacteria that produce only the gene products needed by the cell
- A cell can regulate production of enzymes on 2 levels
  1. *Feedback inhibition* (rapid response)
    - Enzyme inhibited by accumulation of its end product
    - Allows a cell to adapt to short-term fluctuations in the supply of a needed substance
  2. Gene regulation (longer-term response)
    - Transcription of the mRNA coding for the enzyme is switched on or off
- Gene expression in bacteria is controlled by a mechanism described as the *operon model*

# *Operons*

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- A group of functionally related genes can be coordinately controlled by a single “on-off switch”
- The regulatory “switch” is a segment of DNA called an **operator** usually positioned within the promoter
  - Controls access of RNA polymerase to the genes
- An **operon** is the entire stretch of DNA that includes the operator, the promoter, and the genes that they control
- A **repressor** can switch an operon off
  - Prevents gene transcription by binding to operator
  - No repressor = continuous transcription

- 
- A **repressible operon** is one that is usually on
    - Binding of a **repressor** to the operator shuts off transcription
    - Generally function in anabolic pathways
      - Synthesize essential end products from raw materials
  - An **inducible operon** is one that is usually off
    - A molecule called an **inducer** inactivates the repressor and turns on transcription
    - Generally function in catabolic pathways
      - Break down nutrients into simpler molecules



# Gene Expression in Eukaryotes

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- In multicellular organisms, regulation of gene expression is essential for cell specialization
  - Almost all the cells in an organism are genetically identical
  - Differences between cell types result from **differential gene expression**
    - The expression of different genes by cells with the same genome
- A common control point for gene expression is at transcription

# *Chromatin Packing*

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- **Chromatin** is a complex of DNA and protein in the nucleus of eukaryotes
- As a cell prepares for mitosis, its chromatin coils and folds up (condenses)
  - **Histone**
    - Protein around which DNA coils
  - **Nucleosome**
    - Bead-like unit of DNA packing
    - Consists of a segment of DNA wound twice around histones

Figure 13.21a

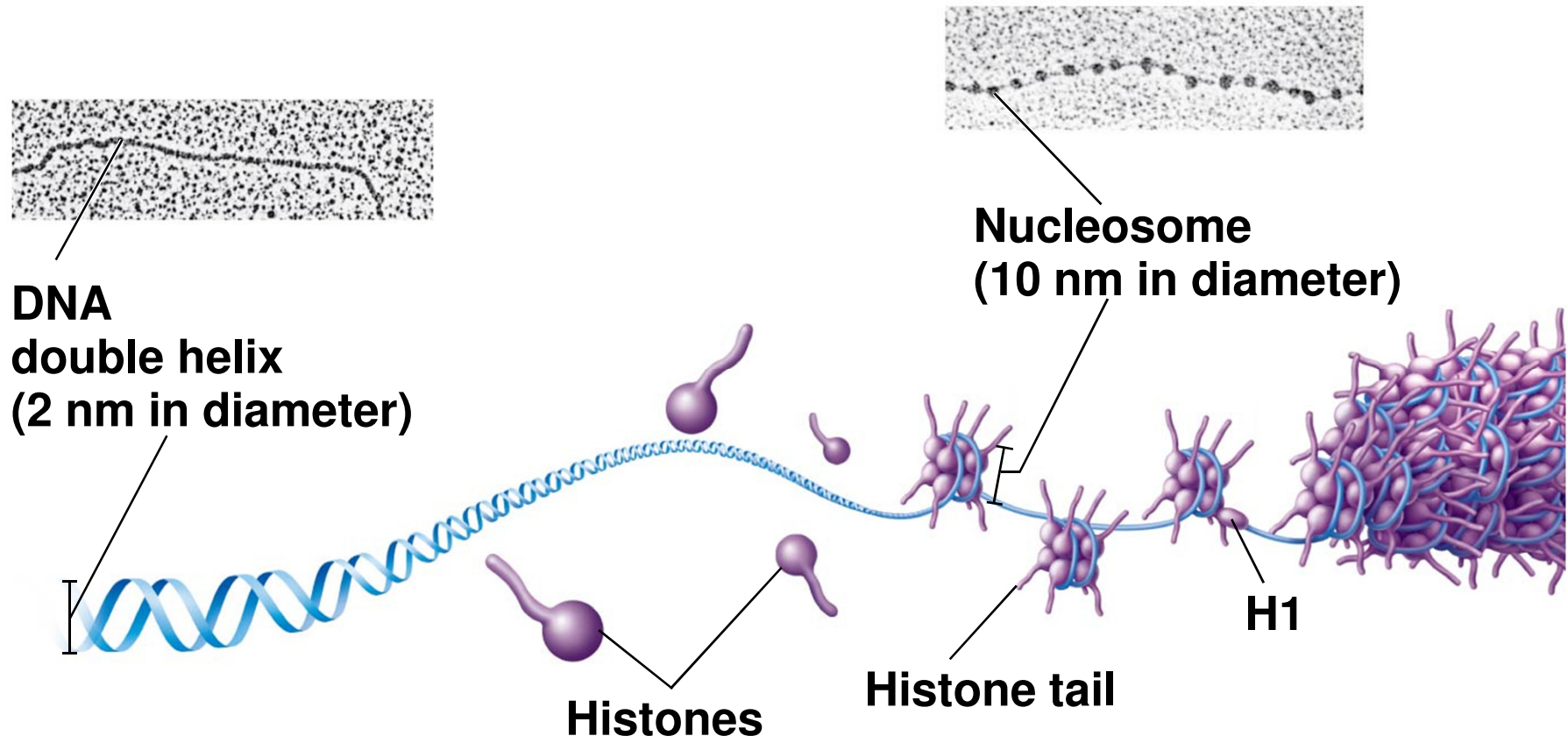
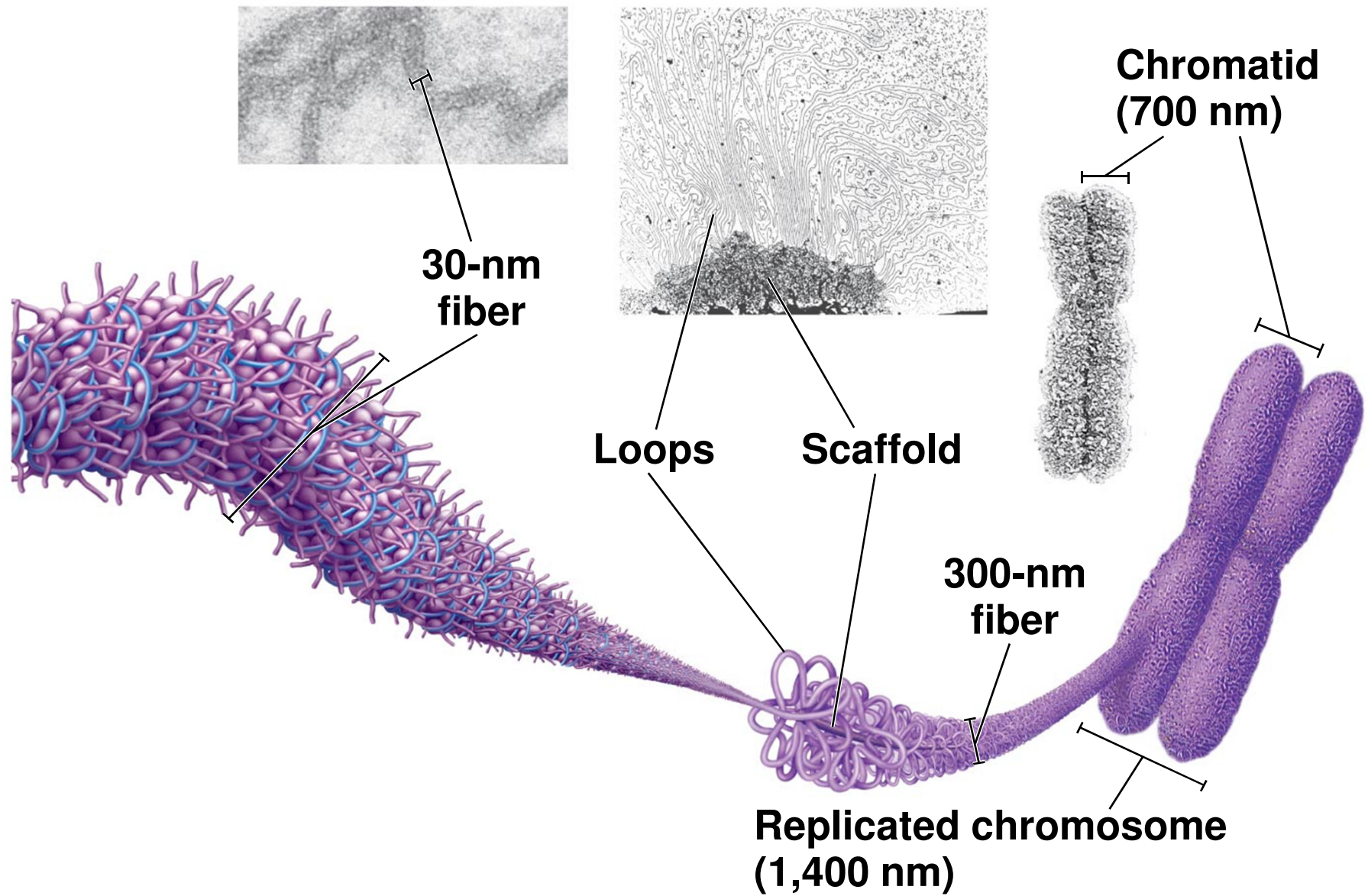


Figure 13.21b



- 
- A condensed region may be loosened or modified as needed for various cell processes
  - Condensed chromatin is called **heterochromatin**
    - Genes within highly condensed heterochromatin are usually not expressed
  - Less compacted chromatin is called **euchromatin**
    - Looser packed euchromatin makes its DNA easier to transcribe
  - **Acetylation** loosens chromatin structure
    - Thus promoting the initiation of transcription
  - **Methylation** can condense chromatin
    - Leads to reduced transcription

# *Transcription Factors*

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- To initiate transcription, eukaryotic RNA polymerase requires the assistance of proteins called **transcription factors**
- Some transcription factors function as
  - **Activators** = bind to an enhancer and stimulate transcription of a gene
  - **Repressors** = inhibit expression of a particular gene

- 
- Genes will be expressed if EITHER
    - Activator is present
    - Repressor is absent
  - Genes will not be expressed if EITHER
    - Activator is absent
    - Repressor is present